SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: SHIBAYAMA, SHIRO
                HIRANO, ATSUSHI
                OHNO, HIROYUKI

    (ii) TITLE OF INVENTION: A NOVEL POLYPEPTIDE AND DNAS ENCODING IT

   (iii) NUMBER OF SEQUENCES: 6

    (iv) CORRESPONDENCE ADDRESS:
         (A) ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
         (B) STREET: 2100 Pennsylvania Avenue, N.W.
         (C) CITY: Washington
         (D) STATE: D.C.
         (E) COUNTRY: U.S.A.
         (F) ZIP: 20037-3202

    (v) COMPUTER READABLE FORM:
         (A) MEDIUM TYPE: Floppy disk
         (B) COMPUTER: IBM PC compatible
         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
         (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
         (A) APPLICATION NUMBER:
         (B) FILING DATE:
         (C) CLASSIFICATION:

   (vii) PRIOR APPLICATION DATA:
         (A) APPLICATION NUMBER: JP 123155/1994
         (B) FILING DATE: 12-MAY-1994

    (ix) TELECOMMUNICATION INFORMATION:
         (A) TELEPHONE: (202)293-7060
         (B) TELEFAX: (202)293-7860
         (C) TELEX: 6491103

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 205 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Gly Thr Ala Gly Ala Met Gln Leu Cys Trp Val Ile Leu Gly Phe
-24              -20              -15              -10
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Leu Leu Phe Arg Gly His Asn Ser Gln Pro Thr Met Thr Gln Thr Ser
            -5                    1               5

Ser Ser Gln Gly Gly Leu Gly Gly Leu Ser Leu Thr Thr Glu Pro Val
        10              15              20

Ser Ser Asn Pro Gly Tyr Ile Pro Ser Ser Glu Ala Asn Arg Pro Ser
    25              30              35                      40

His Leu Ser Ser Thr Gly Thr Pro Gly Ala Gly Val Pro Ser Ser Gly
                45              50                      55

Arg Asp Gly Gly Thr Ser Arg Asp Thr Phe Gln Thr Val Pro Pro Asn
            60              65              70

Ser Thr Thr Met Ser Leu Ser Met Arg Glu Asp Ala Thr Ile Leu Pro
        75              80              85

Ser Pro Thr Ser Glu Thr Val Leu Thr Val Ala Ala Phe Gly Val Ile
    90              95              100

Ser Phe Ile Val Ile Leu Val Val Val Val Ile Ile Leu Val Gly Val
105             110             115             120

Val Ser Leu Arg Phe Lys Cys Arg Lys Ser Lys Glu Ser Glu Asp Pro
            125             130             135

Gln Lys Pro Gly Ser Ser Gly Leu Ser Glu Ser Cys Ser Thr Ala Asn
        140             145             150

Gly Glu Lys Asp Ser Ile Thr Leu Ile Ser Met Lys Asn Ile Asn Met
        155             160             165

Asn Asn Gly Lys Gln Ser Leu Ser Ala Glu Lys Val Leu
170             175             180

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 618 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA to mRNA



        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGGCACCG CAGGAGCCAT GCAGCTGTGC TGGGTGATCC TGGGCTTCCT CCTGTTCCGA        60

GGCCACAACT CCCAGCCCAC AATGACCCAG ACCTCTAGCT CTCAGGGAGG CCTTGGCGGT       120

CTAAGTCTGA CCACAGAGCC AGTTTCTTCC AACCCAGGAT ACATCCCTTC CTCAGAGGCT       180

AACAGGCCAA GCCATCTGTC CAGCACTGGT ACCCCAGGCG CAGGTGTCCC CAGCAGTGGA       240
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AGAGACGGAG GCACAAGCAG AGACACATTT CAAACTGTTC CCCCCAATTC AACCACCATG    300

AGCCTGAGCA TGAGGGAAGA TGCGACCATC CTGCCCAGCC CCACGTCAGA GACTGTGCTC    360

ACTGTGGCTG CATTTGGTGT TATCAGCTTC ATTGTCATCC TGGTGGTTGT GGTGATCATC    420

CTAGTTGGTG TGGTCAGCCT GAGGTTCAAG TGTCGGAAGA GCAAGGAGTC TGAAGATCCC    480

CAGAAACCTG GGAGTTCAGG GCTGTCTGAA AGCTGCTCCA CAGCCAATGG AGAGAAAGAC    540

AGCATCACCC TTATCTCCAT GAAGAACATC AACATGAATA ATGGCAAACA AGTCTCTCA    600

GCAGAGAAGG TTCTTTAA                                                   618
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(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 983 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GCCTGCCCGC CACATACCCA GCTGACATGG GCACCGCAGG AGCCATGCAG CTGTGCTGGG     60

TGATCCTGGG CTTCCTCCTG TTCCGAGGCC ACAACTCCCA GCCCACAATG ACCCAGACCT    120

CTAGCTCTCA GGGAGGCCTT GGCGGTCTAA GTCTGACCAC AGAGCCAGTT TCTTCCAACC    180

CAGGATACAT CCCTTCCTCA GAGGCTAACA GGCCAAGCCA TCTGTCCAGC ACTGGTACCC    240

CAGGCGCAGG TGTCCCCAGC AGTGGAAGAG ACGGAGGCAC AAGCAGAGAC ACATTTCAAA    300

CTGTTCCCCC CAATTCAACC ACCATGAGCC TGAGCATGAG GGAAGATGCG ACCATCCTGC    360

CCAGCCCCAC GTCAGAGACT GTGCTCACTG TGGCTGCATT TGGTGTTATC AGCTTCATTG    420

TCATCCTGGT GGTTGTGGTG ATCATCCTAG TTGGTGTGGT CAGCCTGAGG TTCAAGTGTC    480

GGAAGAGCAA GGAGTCTGAA GATCCCCAGA AACCTGGGAG TTCAGGGCTG TCTGAAAGCT    540

GCTCCACAGC CAATGGAGAG AAAGACAGCA TCACCCTTAT CTCCATGAAG AACATCAACA    600

TGAATAATGG CAAACAAGT CTCTCAGCAG AGAAGGTTCT TTAAAAGCAA CTTTGGGTCC    660

CCATGAGTCC AAGGATGATG CAGCTGCCCT GTGACTACAA GGAGGAAGAG ATGGAATTAG    720

TAGAGGCAAT GAACCACATG TAAATTATTT TATTGTTTCA TGTCTGCTTC TAGATCTAAA    780

GGACACTAGC ATTGCCCCAG ATCTGGGAGC AAGCTACCAA CAGGGGAGAC TCTTTCCTGT    840

ATGGACAGCT GCTGTGGAAA TACTGCCTGC TTCTCCCACC TCCTCAGAGC CACAGGAAAG    900
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AGGAGGTGAC AGAGAGAGAG CAAGGAAAGT GATGAGGTGG ATTGATACTT TCTACTTTGC   960

ATTAAAATTA TTTTCTAGCC TGC   983

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 983 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo sapiens
        (H) CELL LINE: endothelial cell line of umbilical cord vein

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 27..644
        (C) IDENTIFICATION METHOD: by similarity to some other pattern

    (ix) FEATURE:
        (A) NAME/KEY: sig_peptide
        (B) LOCATION: 27..98
        (C) IDENTIFICATION METHOD: by similarity with known sequence or
to an established consensus

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 381..464
        (C) IDENTIFICATION METHOD: by similarity with known sequence or
to an established consensus

    (ix) FEATURE:
        (A) NAME/KEY: mat_peptide
        (B) LOCATION: 99..641
        (C) IDENTIFICATION METHOD: by similarity with known sequence or
to an established consensus

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 312..320
        (C) IDENTIFICATION METHOD: by similarity with known sequence or
to an established consensus

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCTGCCCGC CACATACCCA GCTGAC ATG GGC ACC GCA GGA GCC ATG CAG CTG   53
                          Met Gly Thr Ala Gly Ala Met Gln Leu
                          -24   -20

TGC TGG GTG ATC CTG GGC TTC CTC CTG TTC CGA GGC CAC AAC TCC CAG   101
Cys Trp Val Ile Leu Gly Phe Leu Leu Phe Arg Gly His Asn Ser Gln
-15   -10   -5   1

CCC ACA ATG ACC CAG ACC TCT AGC TCT CAG GGA GGC CTT GGC GGT CTA   149

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                Pro Thr Met Thr Gln Thr Ser Ser Ser Gln Gly Gly Leu Gly Gly Leu
                         5               10              15

AGT CTG ACC ACA GAG CCA GTT TCT TCC AAC CCA GGA TAC ATC CCT TCC                    197
Ser Leu Thr Thr Glu Pro Val Ser Ser Asn Pro Gly Tyr Ile Pro Ser
         20              25              30

TCA GAG GCT AAC AGG CCA AGC CAT CTG TCC AGC ACT GGT ACC CCA GGC                    245
Ser Glu Ala Asn Arg Pro Ser His Leu Ser Ser Thr Gly Thr Pro Gly
    35              40              45

GCA GGT GTC CCC AGC AGT GGA AGA GAC GGA GGC ACA AGC AGA GAC ACA                    293
Ala Gly Val Pro Ser Ser Gly Arg Asp Gly Gly Thr Ser Arg Asp Thr
50              55              60              65

TTT CAA ACT GTT CCC CCC AAT TCA ACC ACC ATG AGC CTG AGC ATG AGG                    341
Phe Gln Thr Val Pro Pro Asn Ser Thr Thr Met Ser Leu Ser Met Arg
             70              75              80

GAA GAT GCG ACC ATC CTG CCC AGC CCC ACG TCA GAG ACT GTG CTC ACT                    389
Glu Asp Ala Thr Ile Leu Pro Ser Pro Thr Ser Glu Thr Val Leu Thr
             85              90              95

GTG GCT GCA TTT GGT GTT ATC AGC TTC ATT GTC ATC CTG GTG GTT GTG                    437
Val Ala Ala Phe Gly Val Ile Ser Phe Ile Val Ile Leu Val Val Val
             100             105             110

GTG ATC ATC CTA GTT GGT GTG GTC AGC CTG AGG TTC AAG TGT CGG AAG                    485
Val Ile Ile Leu Val Gly Val Val Ser Leu Arg Phe Lys Cys Arg Lys
    115             120             125

AGC AAG GAG TCT GAA GAT CCC CAG AAA CCT GGG AGT TCA GGG CTG TCT                    533
Ser Lys Glu Ser Glu Asp Pro Gln Lys Pro Gly Ser Ser Gly Leu Ser
130             135             140             145

GAA AGC TGC TCC ACA GCC AAT GGA GAG AAA GAC AGC ATC ACC CTT ATC                    581
Glu Ser Cys Ser Thr Ala Asn Gly Glu Lys Asp Ser Ile Thr Leu Ile
                150             155             160

TCC ATG AAG AAC ATC AAC ATG AAT AAT GGC AAA CAA AGT CTC TCA GCA                    629
Ser Met Lys Asn Ile Asn Met Asn Asn Gly Lys Gln Ser Leu Ser Ala
             165             170             175

GAG AAG GTT CTT TAA AAGCAACTTT GGGTCCCCAT GAGTCCAAGG ATGATGCAGC                    684
Glu Lys Val Leu  *
             180

TGCCCTGTGA CTACAAGGAG GAAGAGATGG AATTAGTAGA GGCAATGAAC CACATGTAAA                   744

TTATTTTATT GTTTCATGTC TGCTTCTAGA TCTAAAGGAC ACTAGCATTG CCCCAGATCT                   804

GGGAGCAAGC TACCAACAGG GGAGACTCTT TCCTGTATGG ACAGCTGCTG TGGAAATACT                   864

GCCTGCTTCT CCCACCTCCT CAGAGCCACA GGAAAGAGGA GGTGACAGAG AGAGAGCAAG                   924

GAAAGTGATG AGGTGGATTG ATACTTTCTA CTTTGCATTA AAATTATTTT CTAGCCTGC                    983
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(2) INFORMATION FOR SEQ ID NO:5:

25

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 56 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (synthetic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGCTCGTC GACAGATCTG AATTCCATAT GCCCGGGGCG GCCGCACTAG TGGTAC   56

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 56 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (synthetic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACTAGTGCG GCCGCCCCGG GCATATGGAA TTCAGATCTG TCGACGAGCT CCTGCA   56